

Model of a Coral Reef System Polovina, 1984

ECOPATH is a popular network modeling software that is used mainly for created food web networks and simulating the movement of toxins through those systems. In 1984 Jeffrey Polovina designed this ECOPATH model and used data from the French Frigate Shoals in the Northern Hawaiian Islands to run his new model. He used his extensive field work to corroborate the model and produce estimates that were in turn, validated by the collected data.

The ECOPATH model operates using a top-down predator approach. The estimates of the top trophic level organisms are used as a starting point. This model uses a series of ordinary differential equations to simulate metabolism within the specific food web network. The major ODE's in this model consist of biomass production¹, predation mortality², and nonpredation mortality³.

1. $P = \sum_{i=1}^n P_i = \sum_{i=1}^n Z_i B_i$ or $P=ZB$ where P is production, B is the mean annual species group biomass, and Z is the ratio of annual production to mean biomass for a cohort.

2. $R_i DC_{ij} = (b_i + a_i C_i) B_i DC_{ij}$ the predation mortality or the amount of species j consumed by predator species group i

3. $C_i B_i - \sum_{k=1}^n (b_k + a_k C_k) B_k DC_{k1} - d_1 B_1 = 0$ The nonpredation mortality rate.

Using this model a series of ecotrophic efficiencies are calculated. Ecotrophic efficiency (EE) is the fraction of the biomass of that compartment that is used in the system. An EE greater than 1 means that compartment is being consumed more than it is being produced and the model needs to be adjusted. This paper, and this model, has paved the way for food web modeling for years after it was written. ECOPATH is now free, downloadable software that is extremely easy to use. It should be a tool in any food web modelers' arsenal.

Reading Proposal

The paper I would like to propose for class discussion is “Dynamic modelling of honey bee (*Apis mellifera*) colony growth” by Russell et al. (see footnote). As you have probably heard, honey bee colonies have been dying off at alarming rates in recent years. This paper models a colony of honey bees in the hopes of determining which aspects may be most threatened.

Colonial animal population dynamics are interesting because they are affected by both the number of colonies in a population and by the number of individuals in a colony. A colony can almost be thought of as an individual organism because of how highly interconnected it is. Bees specialize on specific tasks, much like organs in an individual, including a single reproductive bee for the entire colony. However, because the colony really is made of individuals, one can still model population dynamics. This paper broadly outlines the lifecycle of a bee. It starts as part of the brood (larvae), transitions into a hive bee (caring for larvae), then transitions into a forager (goes out and collects food). From here, more specific biological details are added to the model. In extreme circumstances where there are not enough hive bees, forager bees can transition back into hive bees. Death can occur at any stage. The number of eggs added to the brood is affected by the number of hive bees. This is a discrete time-model with one-day steps over a period of three years, which includes seasons. Season plays a role in many of the colony dynamics (i.e. forager deaths, maximum eggs laid, incoming food).

They found that the model was most sensitive to the amount of food collected each day, when foraging begins and ends in the year, and the rate of transition from hive bee to forager. This last parameter is affected by a chemical in the brain that can be increased due to hormones, pharmacology, or stress. The model was not particularly sensitive to the death rate of hive bees, implying that parasites or disease within the hive may not have as big of a role as we would have expected.

The vast majority of this paper is an explanation of the model and the reasoning behind the design. As novice modelers, papers like these are interesting and useful to read. This would have been a great model to use for the rebuild project; it was easy to follow along with each step. The connection between parameter sensitivity and biological significance was a significant proportion of the results section. This was an interesting way to use sensitivity analysis that I had not previously considered. Finally, there are aspects of the model that potentially have room for improvement and would make for interesting discussion.

[Stephen Russell, Andrew B. Barron, David Harris, Dynamic modelling of honey bee \(*Apis mellifera*\) colony growth and failure, Ecological Modelling, Volume 265, 10 September 2013, Pages 158-169](#)

Article Title : Time required for sex change in teleost fishes: Hormonal dynamics shaped by selection

http://ac.els-cdn.com/liblink.uncw.edu/S0022519316301953/1-s2.0-S0022519316301953-main.pdf?_tid=9685f502-9a05-11e6-90b5-00000aabb0f26&acdnat=1477326127_cd131278e716a49d7430719d810cfc3e

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The purpose of this model was to assess the role that Cytochrome P450 enzymes play in the feminization or masculinization of hermaphroditic fish species. Based upon social conditions of the fish communities, fish will change gender in order to proliferate at a higher efficiency or to mitigate alterations of the current sex ratio (predation or mortality). The authors noted that in the literature, teleost fishes in harem species appear to transition quicker from female to male than from male to female. The authors then postulate that this could be due to degradation of the P450_{arom}, which converts testosterone into estradiol. The authors then proposed a model examining the role that P450_{arom} plays on sex determination of teleost fish, and compare that model to other game – theory models based upon size –sex differentiation.

I think this paper should be read within our modeling class because of the author's development of the model within a system that is already described by another model (size – advantage hypothesis) and seeks to describe some facets that the previous model could not address in a mechanistic manner. Although the model focuses solely on the interaction between CYP450_{arom} and changes in genders, this model could potentially be used for assessments of other enzymatic functions and their subsequent endocrine responses. Another boon to this paper in relation to this class is that it not only includes lists of other fish species so that the proposed model can be used in a more general fashion, but it also relates the output data of the model back to concepts of evolutionary adaptation as a way to relate the mathematical data back into a biological system. Furthermore, with our class having recently started working with boundaries of systems and understanding forcing variables outside the system of interest, I think this paper tracks well with effects that could be generalized when within the system, or forgotten when excluded from the system that decreases the precision of the model overall.

Model Proposal – Avery Delmaine

“A model for optimization of the productivity and bioremediation efficiency of marine integrated multitrophic aquaculture” demonstrates the use of a model to study multi-species aquaculture with the goal of optimizing production and minimizing net ecological impact on the surrounding environment. The model in this paper uses a series of differential equations to describe nutrient flux between organisms as well as overall biomass gains. The paper then describes the results of a simulation scenario of the model parameterized with salmon, seaweed, and sea urchins as the culture system. The authors do not try to describe all multitrophic aquaculture scenarios in one model, but they propose rather that the framework be used to reparametrize to the specific location and culture species in question.

As the population of people on Earth continues to increase, fish, with high protein levels and low feed conversion ratios compared with many terrestrial animals are good candidates for the large scale production increases needed for feeding demands of this growing population. However, wild fish production has mostly plateaued because for many fish species because people have already maximized harvest rates that allow for suitable fish population recovery that is required for continued harvest. Future increase in world production of fish must come from aquaculture. One problem with large fish culture operations is the nutrient loading on the surrounding environment that often results from the high density of fish, which produce waste, and the decomposition of uneaten feed. A way to combat this problem in marine systems is to simultaneously farm algae and sea urchins in the same system. Algae and urchins in tandem utilize nutrients like nitrogen that the fish culture produces in excess from fish waste, and in turn, less is then loaded into the surrounding environment. An additional bonus is that algae and urchins both provide an economic benefit. To keep the multi-culture thriving, the fish culture must be dense enough to provide enough waste to the other organisms, but not so dense that excess nutrients overload the system and escape into the environment before they can be consumed. Large scale systems with many variables are impractical to test empirically in every possible configuration because of the huge amounts of space, time, and money required. Modeling provides an alternative for understanding the dynamics of these systems.

In short, analyzing the modeling in this paper will allow for an interesting look into nutrient dynamics in a scaled down multi-trophic ecosystem, as well as simultaneously provide a look into possible data driven management of an increasingly important global industry.

Lamprianidou, F., Telfer, T., & Ross, L. G. (2015). A model for optimization of the productivity and bioremediation efficiency of marine integrated multitrophic aquaculture. *Estuarine, Coastal and Shelf Science*, 164, 253-264.

*Access will require log in to UNCW library website so hyperlink **not possible**.

A common problem for fisheries management today is that Marine Protected Areas (MPA's), while effective for long-term sustainability goals, they negatively impact short term yields of fisheries and as such hurt local economies. Brown et al. 2015 compares the short-term profit losses with long term benefits under three scenarios of MPA implementation. The first is gradual implementation (Holland & Brazee, 1996), where a MPA is gradually increased over time. Three plausible policy options for gradual implementation were examined and compared: reserve size, number of species protected, and months per year of reserve closure. To capture the biological component of this study, they used the population dynamics of three species, coral trout (meso-predators), parrotfish (grazers), and snapper (invertivores) as a sample of fish species that are typical of coral reef fisheries, which was the area of focus for the paper, as well as species that may be increased by marine reserves, and they can be selectively harvested for. Fishing effort was held constant over time and the initial conditions for all the simulations were at the equilibrium age structure without reserve.

This model is a two-patch formal model used to describe the population dynamics of fish species in response to fishing and reservations. There were three state variables, each one being a species of fish and assuming no interspecies interactions, influenced by numerous anthropogenic and biological parameters. There were five scenarios run for this model: single reserve implementation, increasing the number of months/year closed to fishing, gradually increasing reserve size, and sequentially protecting species based on value (high-low, low-high, med-low-high). The supplemental material includes the equations and values used for this paper.

I believe this recent paper will both be easily understood with the background the class has given us and enable us to see how the growth models we learned about are integrated with fisheries management. Exploring models such as the ones presented in Brown et al. 2015 will bridge the common trench between scientific research and the socio-economics that drives the main decisions in the country. These models are simplistic enough that there is also room for dynamic discussion about the assumptions made and how they can be improved upon to better represent the interactions of the natural world.

Brown, Christopher J., Sabah Abdullah, and Peter J. Mumby. "Minimizing the Short-Term Impacts of Marine Reserves on Fisheries While Meeting Long-Term Goals for Recovery." *Conservation Letters* 8.3 (2015): 180-189.
+ supplemental materials <http://onlinelibrary.wiley.com/doi/10.1111/conl.12124/abstract>

Baiser 2013 tested the ability of several metacommunity models to predict the structure of the aquatic food webs in populations of purple pitcher plants. The exploratory models included patch-dynamics, species-sorting, mass-effects, and a neutral control, as well as combinations thereof. Model parameters were estimated from regional and local data, and from previous studies. Due to the uncertainty of estimated parameters, specifically the initial dispersal and species interaction coefficients, each model was iteratively run using parameters sampled from observed distributions of potential values. Community dynamics within the pitchers were simulated using generalized Lotka-Volterra differential equations. Resource availability was simulated using linear and non-linear forcing variables. The metacommunity model determined the presence or absence of each species in the community. The accuracy of each model was assessed by comparing the predicted structures from the model to empirical measurements from three pitcher plant communities.

This paper builds upon familiar community modelling techniques and demonstrates the function of these techniques in metacommunity models. At its core, these metacommunity models rely on community models that we've already encountered: population dynamics were modelled using predation differential equations and resource availability was modelled using forcing data. Similarly to how we've compared these community models in lecture, this paper compares the dynamics of several metacommunity models in a natural extension of the base community model.

The value of this paper extends beyond developing and implementing metacommunity models: it's a paradigmatic example of the process of practical science. For each model, sensitivity analyses were used to quantify accuracy, providing a practical example of how to incorporate uncertainty into deterministic models. And, although the models developed in this paper are not perfect, the authors demonstrate that incomplete models can guide future studies.

The implications of these results for ecological theory and modelling are also important aspects of this paper. This paper provides a theoretical framework for how both community and metacommunity dynamics influence food web structure and examines the specific limitations of the proposed models. Another distinction is the approach of using pitcher plants as natural microcosms. By using a small, standardized ecosystem, this authors retain the potential to eventually test these theories experimentally. If a larger ecosystem was modelled instead, the experimental approach may be more difficult logistically. Finally, the use of network indices as a standard by which to compare ecosystems illustrates a shift towards measuring the environment using comprehensive measurements of ecosystems rather than specific measurements of individual populations. This shift reflects an understanding that, although the abundances of individual species may be difficult to accurately predict, there are fundamental, measurable properties of whole ecosystems that may be more reliable.

This paper is an excellent combination of old and new modelling techniques, allowing us to readily put these new techniques in the context of what we've previously learned. This paper also highlights a potential application of modelling beyond population dynamics by using natural microcosms as a unit of study and by incorporating metrics that describe entire food webs. These models yield valuable insights into how ecosystems function and exemplify the role of modelling in understanding ecosystem processes.

Baiser, B. B. (2013). [Predicting food-web structure with metacommunity models](#). *Oikos*, 492-506.